

**RAW SEQUENCE LISTING
ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH

RECEIVED

JAN 08 2001

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/383,789A

Source: 1653

Date Processed by STIC: 12/28/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 08/383,789A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleic The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 Use of <213>Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
1-4

12 Use of <220>Feature (NEW RULES) Sequence(s) are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

RECEIVED

JAN 08 2001

TECH CENTER 1600/2900

RECEIVED 1653

JAN 08 2001

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/383,789A

DATE: 12/28/2000
 TIME: 08:06:47

Input Set : A:\X-12013.txt
 Output Set: N:\CRF3\12282000\I383789A.raw

TECH CENTER 1000-2000
 Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Hughes, Benjamin
 4 Wolff, Ronald
 6 <J20> TITLE OF INVENTION: METHOD FOR ADMINISTERING INSULINOTROPIC PEPTIDES
 8 <130> FILE REFERENCE: X-12013
 10 <140> CURRENT APPLICATION NUMBER: 09/383,789A
 11 <141> CURRENT FILING DATE: 1999-08-26
 13 <150> PRIOR APPLICATION NUMBER: US 60/098273
 14 <151> PRIOR FILING DATE: 1998-08-28
 16 <150> PRIOR APPLICATION NUMBER: US 60/100012
 17 <151> PRIOR FILING DATE: 1998-09-11
 19 <160> NUMBER OF SEQ ID NOS: 4
 21 <170> SOFTWARE: PatentIn version 3.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 29
 25 <212> TYPE: PPT
 26 <213> ORGANISM: Artificial/Unknown
 28 <220> FEATURE:
 29 <221> NAME/KEY: PEPTIDE
 30 <222> LOCATION: (1)..(1)
 31 <223> OTHER INFORMATION: X at position 1 is Ala, Gly, Val, Thr, Ile and alpha-methyl-Ala. (Genus/species)
 34 <220> FEATURE:
 35 <221> NAME/KEY: PEPTIDE
 36 <222> LOCATION: (14)..(14)
 37 <223> OTHER INFORMATION: X at position 14 is Glu, Gln, Ala, Thr, Ser and Gly.
 40 <220> FEATURE:
 41 <221> NAME/KEY: PEPTIDE
 42 <222> LOCATION: (20)..(20)
 43 <223> OTHER INFORMATION: X at position 20 is Glu, Gln, Ala, Thr, Ser and Gly.
 46 <400> SEQUENCE: 1
 48 Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Xaa Gly Gln
 49 1 5 10 15
 51 Ala Ala Lys Xaa Phe Ile Ala Trp Leu Val Lys Gly Arg
 52 20 25
 54 <210> SEQ ID NO: 2
 55 <211> LENGTH: 29
 56 <212> TYPE: PRT
 57 <213> ORGANISM: Artificial/Unknown
 59 <220> FEATURE:
 60 <221> NAME/KEY: PEPTIDE
 61 <222> LOCATION: (28)..(28)
 62 <223> OTHER INFORMATION: X at position 28 is Lys
 65 <220> FEATURE:
 66 <221> NAME/KEY: PEPTIDE
 67 <222> LOCATION: (29)..(29)
 68 <223> OTHER INFORMATION: X at position 29 is Gly or is absent
 71 <400> SEQUENCE: 2
 73 His Ala Glu Gly Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly

pp 1-2
 Per 1.823 of new Sequence Rules, the
 only valid <213> responses are: Unknown,
 Artificial Sequence, or Scientific name
 (Genus/species)

one of the
 three - do not
 combine responses

(see item 12 on
 Error Summary
 sheet)

OK

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/383,789A

DATE: 12/28/2000
TIME: 08:06:47

Input Set : A:\X-12013.txt
Output Set: N:\CRF3\12282000\I383789A.raw

RECEIVED

JAN 08 2001

TECH CENTER 10002000

OK 74 1 5 10 15
76 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Xaa Xaa
77 20 25
79 <210> SEQ ID NO: 1
80 <211> LENGTH: 29
81 <212> TYPE: PRT
82 <213> ORGANISM: Artificial/Unknown
84 <220> FEATURE:
85 <221> NAME/KEY: PEPTIDE
86 <222> LOCATION: (19)..(19)
87 <223> OTHER INFORMATION: X at position 19 is Lys or Arg.
90 <400> SEQUENCE: 3
92 Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln
93 1 5 10 15
OK 95 Ala Ala Xaa Glu Phe Ile Ala Trp Leu Val Lys Gly Arg
96 20 25
98 <210> SEQ ID NO: 4
99 <211> LENGTH: 31
100 <212> TYPE: PRT
101 <213> ORGANISM: Artificial/Unknown
103 <220> FEATURE:
104 <221> NAME/KEY: misc_feature
105 <222> LOCATION: ()..()
106 <223> OTHER INFORMATION: Description of Artificial Sequence
109 <400> SEQUENCE: 4
111 His Val Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
112 1 5 10 15
114 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
115 20 25 30

VERIFICATION SUMMARY
PATIENT APPLICATION: US/09/383,789A DATE: 12/28/2000
TIME: 08:06:48

Input Set : A:\X-12013.txt
Output Set: N:\CRF3\12282000\I383789A.raw

L:48 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:51 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

RECEIVED

JAN 08 2001

TECH CENTER